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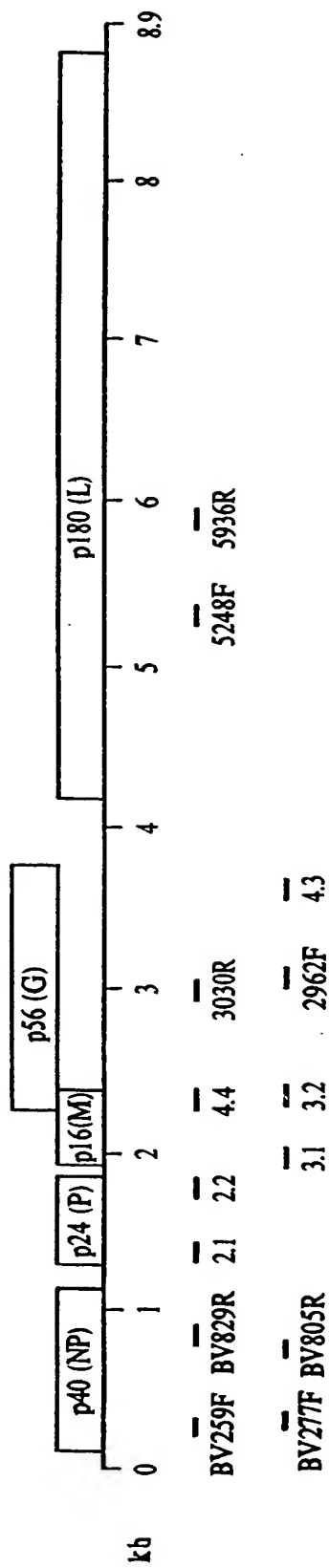


FIG. 1



Cons nsus	90	GTTGGTTAAACAACCAATCATYATYCTTCTAACAATAATGAACACACGCAATGCCACCCAAAGAGACGCTGGTTGATGACGCCGATG
BDV JCT	90A...T..C.....
BDV Briese	90C...C...T.....
Consensus	180	CCATGGAGGAYCAAGATYATATGAACCCCGAGCGCTCCCYAAGCTCCCYGGRAAATTCCTACAATACACCGTTGGGGGGTCTGACC
BDV JCT	180C...T.....
BDV Briese	180T.....C.....
Consensus	270	CGCATCCGGGTATAGGGCATGAGAAAGAYATCAGGCAGAACCGAGTGGCATGTGTAGACCAGTCACGGGGCGGATATGTTTCAYACAGTAA
BDV JCT	270G..T.....
BDV Briese	270A..C.....
Consensus	360	CGCCYAGCCTTGTTCTATGTTTGCTAATCCCAGGACTGCACGCTGCCGTTGTTCCAGGAGGGTGCCCTCGTGAATCYTACCTGTGCGA
BDV JCT	360C.....
BDV Briese	360T.....
Consensus	450	CGCCTGYACGGTGGRGAAACAGACTGYGTTAAGACTGCRAAGTTTACGGGGAAAGACRACRACGCGTGATCTCACCAGAGCTGGAGA
BDV JCT	450T.....G.....C.....
BDV Briese	450C.....A.....T.....G.....
Consensus	540	TCTCCTCTATMTTCAGCCATTGTTGCTCATTACTAATWGGGGTGTGATAGGATCGTCTCTAAGATYAAAGCAGGAGCCGAGCAGATCA
BDV JCT	540A.....
BDV Briese	540C.....
Consensus	630	AGAAAGGTTTAAACTATGATGGCAGCCTTAAACCGGCCATCCCATGGTGAGACTGTACACTACTYCACAGATGTTTAAATCCACATGAGG
BDV JCT	630
BDV Briese	630

FIG. 2A

Consensus	CTATAGATTGGATTAAACGGCCARCCCTGGGTAGGCTCCTTTGTGTGTCTCTACTACAGACTTTTGAGTCCCCAGCTAAAGAATTYA	720
BDV JCTG.....A.....	720
BDV BrieseT.....	720
Consensus	TGGAYCAGATTAAARCTTGTTCGCAAGTTATGCRACAGATGACTAGCTACACTACTATAAAGGAGTACCTCGCAGAATGYATGGATGCTACCC	810
BDV JCTT.....A.....G.....	810
BDV BrieseC.....G.....A.....	810
Consensus	TTACAATCCCCTAGTTCATATGAGATYCGTGACTTTTTAGAAGTTTCAGCAAGCTTAARGAGGAWCATGCTGACCTGTTTCGGTTC	900
BDV JCTT.....T.....	900
BDV BrieseC.....C.....	900
Consensus	TGGGGGCYATTMGRCAACCCCGACGCTATCAAGCTKGGCCACGRAGCTTCCCAATCTGGCTCYGCAGCGTTTACTGGAGTAAAGAAGG	990
BDV JCTT...C.G.....T.....G.....	990
BDV BrieseC...A.A.....G.....A.....	990
Consensus	ARAYCCACAATGGCRGGCTACCGGGCCTCCACCATCCAGCGGGGGRAGTGTCAAGGARACCCAGCTGCCCGGTATAGGCCCGCGG	1080
BDV JCT	.G..T.....G.....	1080
BDV Briese	.A..C.....A.....	1080
Consensus	AGATATCTCGYGGRGARGACGGGCAGAGCTCTCAGGTGAGATCTCTGCCATAATGARRATCATAGGTGTGACTGGTCTAAACTARAAAA	1170
BDV JCTC..G..A.....	1170
BDV BrieseT..A..G.....	1170
Consensus	CAATGAACAAACCAATAAAAAACCAAAATGGCGCAACCCYCCGGACCTGYGATGAGYTCCGACCTCCGGCTGACATGCTTGAAYTAGT	1260
BDV JCTC.....	1260
BDV BrieseT.....C.....	1260
Consensus	CAGGAGGCTCAATGGCAACGCGACCATCGAGTCTGGTGGACTCCCTGGAGGACGAGAGAGATCCCCAGACACTACGACGGGAACGAYCGG	1350
BDV JCTG.....	1350
BDV BrieseC.....	1350

FIG. 2B

Consensus	GGTCACCAAGACCCAGGAAGRTCCCAAGGAATGCATTGACCCACCRGTAGACAGCTCCTGAAGGACCTCAGGAAGAACCCCTCCATGA	1440
BDV JCTA.....G.....	1440
BDV BrieseG.....A.....	1440
Consensus	TCTCAGACCCAGACCGAACCAGGAGCAGCTRTTCGAATGATGAGTWTATCAAGAAGYTACTGACGGAGCTGGCCGAGAAATAGCA	1530
BDV JCTA.....T.....C.....	1530
BDV BrieseG.....A.....T.....	1530
Consensus	TGATCGAGGCTGAGGAGGTGCGGGGCACCTCTTGGRGACATCTCGGCTCGYATCGAGGAGGGTTTGAGTCCCTGTCCGCCCTCCAATGG	1620
BDV JCTG.....C.....	1620
BDV BrieseA.....T.....	1620
Consensus	AAACCATCCAGACAGCTCAGCGGTGCGAYCACTCCGAYAGCATCAGRATCCTYGGGAGAACATCAAGATACTRGATCGTCCATGAAGA	1710
BDV JCTC.....T.....A.....T.....G.....	1710
BDV BrieseT.....C.....G.....C.....A.....	1710
Consensus	CAATGATGGAGACAATGAAGCTCATGATGGAGAGGTGGAYCTCCTCTACGCATCAACCGCCGTTGGGACCTCTGCACCCATGTTGCCCT	1800
BDV JCTC.....	1800
BDV BrieseT.....	1800
Consensus	CCCATCCTGCACCTCCGGGCATTATCCCCAGCTCCCAAGTGCCCCGACARCGGATGARTGGGACATCATACCATAAAAAAATCGAATCA	1890
BDV JCTG.....G.....	1890
BDV BrieseA.....A.....	1890
Consensus	CCATGAATTCAAARCATTCCTATGTGGAGCTCAAGRCAAGGTAATCGTCCCTGGATGCCCCACACTGATGCTTGAGATAGACTTTGTAG	1980
BDV JCTG.....	1980
BDV BrieseA.....	1980
Consensus	GRGGGACTTCACGGAACCACTTCCTTAACATCCCATTCTTTTCAGTGAAGAGCCCTCTGCAGCTTCCACGCCGAGAGAGTTGACCGACT	2070
BDV JCT	.A.....	2070
BDV Briese	.G.....	2070

FIG. 2C

Consensus	ACTTYACVATTGACGTAGARCCAGCAGGTCAATCCCTGGTCAAYATATACTTCCAGATTGACGACTTCTTGTCTCCTAACACTCAACTCAC	2160
BDV JCTC..C.....G.....C.....T.....	2160
BDV BrieseT..T.....A.....T.....	2160
Consensus	TRTCYGRFTACAAGGACCCGATTAGRAAATACATGTTCTACGGCTCAACAAGGAMCAGAGCAAGCAGCAATYAATGCAGCYTTCAATG	2250
BDV JCT	.G..C..A.....G.....A.....A.....T.....	2250
BDV Briese	.A..T..G.....A.....C.....C.....C.....	2250
Consensus	TCTTYTCTTATCGGCTTCGGAACATTGGTGTGGYCCCTCTCGGCCCGACATTCGATCTTCAGGGCCTTAGYTGCAATACTGACTCCACT	2340
BDV JCTC.....C.....T.....G.....T.....	2340
BDV BrieseT.....T.....G.....C.....C.....	2340
Consensus	CCTGGAYTRATYGAICTGGAGATAAGGCGACTTGGCCACACCCCAACGGAAATGTCATTTTCATGGGAGTTAGTTATCTCTYAACCACACG	2430
BDV JCTT..A..C..T.....G.....A.....T.....	2430
BDV BrieseC..G..T..C.....C.....C.....C.....	2430
Consensus	ACTATTAGCCTCCGGCAGTCCACACRATCATGCCTCAAGTACCACCTGCAAAACCTATTGGGGATTCTTTGGTAGCTACAGCGCTGACCGA	2520
BDV JCTG.....A.....C.....C.....	2520
BDV BrieseA.....C.....C.....C.....	2520
Consensus	ATCATMAATCGGTACACTGGTACTGTTAAGGGTTGTGTAAACAACCTCAGCRCCAGAGGAYCCCTTCGAGTGCAACTGGTTCTACTGCTGC	2610
BDV JCTC.....T.....G.....T.....	2610
BDV BrieseA.....C.....A.....C.....C.....	2610
Consensus	TCGGCGATTACAACAGAGATCTGCCGATGCTCTATTACAAATGTACGGTGGCTGTRCARACATTCACCAGTTTCATGTACTGCAGTTTY	2700
BDV JCTA..G.....C.....	2700
BDV BrieseG..A.....A.....T.....	2700
Consensus	GCRGACTGYAGTACYGTGAGYCARCAGGAGCTAGAGAGTGGMAAGGCAATGCTGAGCGATGGCAGTACMTTACTTATACCCCGTATATC	2790
BDV JCT seq	..G....T....T....T..G.....C.....C.....	2790
BDV Briese	..A.....C.....C.....C..A.....A.....A.....A.....	2790

FIG. 2D

Consensus	ACGAGGCTGAYCTCCTTCCATACACACAGGTCTAGTAATATAACRTCTACRGATACAGGCTCAGGCTGGTGACATCGGCTACCCCTCA	3600
BDV JCTC.....T.....G.....A.....G.....	3600
BDV BrieseT.....A.....G.....	3600
Consensus	TTTGCTTCCCTCAATCCYCTCGGGTGGCTYAGGACCTACTTGRTGGGRGCCTGGTGGTGGGGTCTTACTATAAAGTCTTTGT	3690
BDV JCTT.....C.....T.....G.....A.....	3690
BDV BrieseC.....C.....A.....A.....	3690
Consensus	GTTTCCTTACCAGCCTCCTTCGGGAGGAGAGCGCCTCGGCGGTGGCAGGAATAAACCGTACCGACCARNCTCTTAAAAACCCCTCTYC	3780
BDV JCTAA.....GT.....C.....	3780
BDV Briese	3780
Consensus	TCGGRACAGAGGTCTCTTTCTGCCCTTAARTCGAGYTCACCTCCCCCATCAYGTCAGGACAYTRGCCCAGATTAAAGCAARGAACCTGGCAT	3870
BDV JCTG.....A.....T.....C.....T.....G.....A.....	3870
BDV BrieseA.....G.....C.....T.....C.....A.....G.....	3870
Consensus	CCTGTGACTATTACTTGTCTATTCCCGCCAAGTTGTATTGGCCCTGAAGTATATCCCATTTGGTGTYYTATAAGAGCTGCGGAGGCYATAC	3960
BDV JCTCT.....TC.....T.....	3960
BDV Briese	3960
C nsensus	TAAACAGTTATAGTATCAGCTTGGAAAGCTGGATCAATGACRAAGACCCTATATCTCTGTGAGATATGCACTCACCAATCCCGGGGTCC	4050
BDV JCTC.....A.....G.....	4050
BDV BrieseT.....G.....	4050
Consensus	GRGCCCAACTTGAGCTYCACATTGCGCTACCAGGCATAGTGGGTCAAGTCTCGTAYAGCCGGGARGCAGAYATAGGGCCAAAGGCTTG	4140
BDV JCTG.....C.....T.....T.....A.....T.....	4140
BDV BrieseA.....T.....C.....G.....C.....	4140
Consensus	GGAATATGTCATTGCAATTCAATCYCTCGTTATTGGCCACCATAGACACRACRAGCTGCCTAATGACCTACACCACCTTCTTGCTG	4230
BDV JCTC.....A.....G.....	4230
BDV BrieseT.....G.....A.....	4230

FIG. 2F

Consensus BDV JCT BDV Briese	CAGCAGACACAGCCAAGAGCAGATGCCAYCTCCTAATCGCCTCAGTGGTCCARGGRGCCCTTTGGGARCAAGGTCATTCTTGTATCATAC.....A.A.....G.....T.....G.G.....A.....	4320 4320 4320
Consensus BDV JCT BDV Briese	TAATCAACATGATCGACAYAAATTGACTCAATCAACCTCCCCATGATGATTACTTCACAATTATTAAAGTCTATCTYTCCTACTCCCAAGC.....T.....	4410 4410 4410
Consensus BDV JCT BDV Briese	GGCTTGTTATGGGGAGGCAAYAATGTRTCAGTCTCCTCTGATTYGGTCCGTATTTCYATTCCTGAATYATGCCCRCAACTAGACAGCTC.....G.....T.....A.T.....C.....A.....T.....A.....C.....G.C.....T.....G.....	4500 4500 4500
Consensus BDV JCT BDV Briese	TACTAAAAAACTGCTYCAACTTGACCCYGTTCCTCCTCATGGTCTCTTCGGTGCAGAAGTCATGGTACTTCCTCAGATCCGAATGGT.....T.....C.....C.....	4590 4590 4590
Consensus BDV JCT BDV Briese	TYGACGGGTACACGGGAGCAGCTCCACAAGATGCGTGTGAGCTGGARACGCCCAAGCCCTGCTGTCTAGGGCCATACCCCTCCTGTCAA ..T.....G.....A..... ..C.....A.....G.....	4680 4680 4680
Consensus BDV JCT BDV Briese	TATTCGRGCAGAGTTTATCAAGGCTATGTCTCAAGAATGCGAAGTGGCCGCCCYGTACACCTGCTCCAGGCTGTGACAAATCCATAAA.....T.....C.....G.....	4770 4770 4770
Consensus BDV JCT BDV Briese	ARAATGCGAGAGCTGGGCCGCTGAGCCCGGYRTTGTGACCGAGGATGGCAGCTCTTCGMAAGGTTGTTCATTCTAAGAATTGCTGACC ..G.....TG.....CA.....A..... ..A.....	4860 4860 4860
Consensus BDV JCT BDV Briese	TAGATATGGATCCCGACTTCAACGATATTGTTAGCGAYAAGGCGATAATCAGCTCAAGAAGGACTGGGTATTYAGTACAAATGCAGCRGC.....T.....C.....G.....	4950 4950 4950

FIG. 2G

Consensus	CCTTTTGAAGAAATACRGTGARCGGTTGGAGAGGCCCYCCTGCCAGRTCGGAGCCRTCACGRCTTGTGTAATGCTCTRATCGATGGAGCCT	5040
BDV JCTA...G.....C.....A.....A.....G.....G.....	5040
BDV BrieseG...A.....T.....G.....G.....A.....A.....	5040
Consensus	TAGAYAAATATCCAGCCCTGCTAGAGCCATTTTACAGGGGAGCGGTTGAGTTYGAGGATCGGYTCACTGTGCTCGTGCCCTAAGGAGAARG	5130
BDV JCT	...T.....C.....T.....C.....T.....C.....	5130
BDV Briese	...C.....C.....T.....A.....	5130
Consensus	AGTTRAAGGTAAAGGCAAGGTTCTTCTCGAAGCAACATTTGGCAATCAGGATATATACAGGTTGTGCTGAAGCTGCACCTTAAGAAAYGAGG	5220
BDV JCT	...G.....A.....	5220
BDV Briese	...A.....T.....	5220
Consensus	TTATGCCATACYTAAARACACAYTCAATGACCATGAGCTCAACGGCYCTAACYCAYCTTCTTAACGGGCTATCACATACTATCACAAGG	5310
BDV JCTT...A...T.....C.....C...C...T.....C.....	5310
BDV BrieseC...G...C.....C.....T...T...C.....	5310
Consensus	GTGACTCCTTTGTATTAAACYTWGAYTATAGYTCCTGGTGCAACGGTTCCGACACAGACTRCARGCCCCCANTCTGTCGTCAGTTGGATC	5400
BDV JCTT.A..T...C.....A.....A.....C.....	5400
BDV BrieseC.T..C...T.....T.....G..G.....A.....	5400
Consensus	AGATGTTCAATTGCGGGTACTTCTTCAGGACTGGGTGCACACTGCCATGCTTACCAGGTTTATTATTCARGACAGRTTCAACCCGCCCT	5490
BDV JCTG.....A.....	5490
BDV BrieseA.....G.....	5490
Consensus	ATTCCYTCMGTGTGAGCCCGTTGAAGACGGWGTACATGCCGGTTGGGACTAARACAATGGGRGAGGGYATGAGGCAGAAAATATGGA	5580
BDV JCTT..C.....T..C.....G.....A...T.....	5580
BDV BrieseC..A.....A..T.....A.....G...C.....	5580
Consensus	CAATYCTTACGAGCTGCTGGGAGATAATTGCTCTTCGGGAAATTAAACGTGACGTTTAAATATACTAGGCCARGGTGATATATCAGACAATCA	5670
BDV JCTT.....T.....C.....	5670
BDV BrieseC.....A.....	5670

FIG. 2H

Consensus	TYRTACATAAATCTGCAAGCCCAAAATAAAYCAGCTATTAGCGGAGCGAGCAYTRGGRGCTYTTGTACAGCATGCTAGATTAGCTGGCCATA	5760
BDV JCT	.TG.....T.....T.....T.G.A..TT.....	5760
BDV Briese	.CA.....C.....C.A..G..CC.....	5760
Consensus	ACCTYAAGGTAGARGAATGYTGGGTGCAGATTGTCTGTATGAGTATGGAAGAAGCTYTTCTTCCTGGTGACCTGTCCCRGGCTGTT	5850
BDV JCTT.....A.....T.....C.....C.....	5850
BDV BrieseC.....G.....C.....T.....T.....G.....	5850
Consensus	TGAAGCAGCTCTCRCGGGTGACGGGAYTCYACTGGRGAGYTATTCCCAAACCTATACTCAAAGTTAGCCTGCTTAACATCATCTGYTTAA	5940
BDV JCTG.....G.....C..C.....G..T.....	5940
BDV BrieseA.....A.....T..T.....A..C.....	5940
Consensus	GCGCAGCGATGGCAGACACATCYCCATGGGTGGCACTCGCGACAGGTGTCTGTCTGTATCTTATCGAGTTRTATGTTGAGCTGCCCTCCRG	6030
BDV JCTC.....C.....T.....	6030
BDV BrieseT.....T.....A.....G.....C.....	6030
Consensus	CAATCAGCAGGAYGAGTCGCTRTTRACGACCCCTCTGYCTCGFAGGYCCATCCATTGGTGGGCTTCACACCTGCTGCAACCTRCCCAGTG	6120
BDV JCTC.....G..A.....T.....T.....A..T.....G.....	6120
BDV BrieseT.....T.....A..G.....C.....C.....G..C.....A.....	6120
Consensus	TCTTTTTCAGAGGAATGTCGAGACCCAYTGCCCTTTCAGCTAGCACTCTTGACAGACCCCTCATTAARACGACAGGGGTGACYTGTAGCTTGG	6210
BDV JCTT.....C.....	6210
BDV BrieseC.....C.....G.....	6210
Consensus	TGAATCGTGTGTYAAGTTACGGATAGCACCCCTATCCAGACTGGCTCTCYCTAGTGACTGACCCGACCTCACTCAACATGTCYCARGTGT	6300
BDV JCTT.....C.....G.....C.....T.....T.....G.....	6300
BDV BrieseC.....C.....T.....C.....C.....C..A....	6300
Consensus	ACCGGCCAGAACGTCARATCAGGAGGTGGATTGAGGARGCRATAGCRACAAGCTCACACTCGTCACGCATAGCAACTTYYTTCACGAGS	6390
BDV JCTA.....G.....G..A.....A.....G.....T.....G.....	6390
BDV BrieseG.....G.....A..G.....G.....C.....C.....C.....	6390

FIG. 21

Consensus	CCCTCACGGAGATGGCYCAGYTGCTTGCAGGAGCACCTYTCAACAATGATGCCTCTTCGRCCCGGGGATATGTGGCCTTATTTCGCATTAT	6480
BDV JCTC...C.....C.....G.....	6480
BDV BrieseT...T.....T.....A.....	6480
Consensus	CAAATGTCCGATAYGGTYTAAGCATATAGATCTATTTCAAAARTCCCTCTACCGTTGTYTCTGCAAGTCAAGCTGTCCATATCGARGATG	6570
BDV JCTT...C.....G.....C.....A....	6570
BDV BrieseC...T.....A.....T.....G....	6570
Consensus	TTGCCCTAGAGAGTGTAAAGGTATAAGGAATCTATCATYCAAGGCTCTGTAGACACYACTGAGGGGTAYAACATGCAACCTTATTGGGAAG	6660
BDV JCTT.....C.....T.....C.....	6660
BDV BrieseC.....C.....T.....	6660
Consensus	GTTGCACCTTACCTTGCAGCCCAARCAGYTACGKAGGTTGACRTGGGGTCGAGACCTAGTTGGAGTYACATGCCGTTGTGCCGAGCAAT	6750
BDV JCTG...C...G.....G.....T.....	6750
BDV BrieseA...T...T.....A.....C.....	6750
Consensus	TCCATCCYCAYAGTTCTGTSGGTGCAAAARGCRGAACCTCTACCTCGAYCTATYATATACTCCCCACARGAGACRWTGCGGTCCACACCATC	6840
BDV JCTC..T.....C.....A..A.....T...C.....A...G.....	6840
BDV BrieseT..C.....G.....G...G.....C...T.....G...A.....	6840
Consensus	TGACTACCAGGGGGACCCGCTTTACCTYGGATCYAATACGGCTGTCCAMGGTYCAGCGAGGTGAGATCACRGGCCTAACAAAGTCAA	6930
BDV JCTT.....T.....C...T.....C...T.....A.....G.....	6930
BDV BrieseC.....C.....A...C.....G.....	6930
Consensus	GGGCTGCAAAATCTAGTCARGGACACTCTCGTTCTCCAYCAGTGGTYAARGTCCGTAARGTTACCGATCCACACTTGAACACYCTCATGG	7020
BDV JCTA.....G.....C.....C...G.....G.....T.....	7020
BDV BrieseG.....T.....T...A.....A.....C.....	7020
Consensus	CRCGCTTCTTRCTTGAGAAGGGTACACATCTGACGCTCGRCCTAGCATYCAGGGTGGGACCCTCACRCAATCGTCTCCCATCCCGYGGAG	7110
BDV JCT	.G.....G.....A.....G.....T.....A.....	7110
BDV Briese	.A.....A.....G.....A.....C.....G.....C.....	7110

FIG. 2J

Consensus	ACTCAGSCARGGGCTYACTGGGTATGTRAAATATACTMAGYACGTGGCTYCGRTTCTCAAGTGATTATCTTCACTCTTTCTCGAAATCAT	7200
BDV JCTC..A.....C.....G.....C..C.....C..G.....	7200
BDV BrieseG..G.....T.....A.....A..T.....T..A.....	7200
Consensus	CAGAYGACTAYACAATCCACTYACGATGTATTACATACGGTTGCCCTCTATGCTGATTCCGGTGATTAGATCGGGCGGTGTATTTCGA	7290
BDV JCTT.....C.....C.....	7290
BDV BrieseC.....T.....	7290
Consensus	CTCCTTACCTTTTGAGTGCAAGTTGTAAACATGCTTTGAGAAGATAGACTCAGAGGAGKTCGTCTCTGGCATGYGAACCYCAATAYAGGG	7380
BDV JCT	7380
BDV Briese	7380
Consensus	GTGCTGAGTGGCTGATATCAAGCCAGTYACTGTCCCTGAGCAGATAAYTGAYGCTGAAGTCGAGTTTGACCCCTGTGTGAGTGCGRGTT	7470
BDV JCTT.....T.....T..C.....	7470
BDV BrieseC.....C.....T.....	7470
Consensus	ATTGTCTCGGGATTCTCATTTGGCAAGTCATTCCTTRGTTGACATAAGGGCAACTGGGCATGATATYATGGAGCACGGGACATGGGGCTAACY	7560
BDV JCTG.....A.....	7560
BDV Briese	7560
Consensus	TGGAGAGGTTTCTGTRTCGGACATGCAGAAACTTCCTRTGGAGTATTGTAATTCGGTCTCTCTGGAGATTCCCTATTGGCGCACGRCTCC	7650
BDV JCTG.....A.....	7650
BDV BrieseA.....G.....	7650
Consensus	TYCAGTTTGAGAAGGCTGGCCTYATTAGRATGCTGTATGCTGCRACAGGTCCAACCCYTAGCTTCCTAATGAAGTYTTTCAAGACTCAG	7740
BDV JCT	.C.....T.....G.....A.....A.....TT.....C.....	7740
BDV Briese	.T.....C.....A.....G.....CC.....T.....	7740
Consensus	CCCTMCTYATGGACTGGCAGCCYCTYATCGGCTGTMCCTAGATCAACTTTCATAGTCGGGAGACCTCGTYGCTYAGCTYGTATTAT	7830
BDV JCTA..T.....T..T.....A.....	7830
BDV BrieseC..C.....C..C.....C.....T..T.....T.....	7830

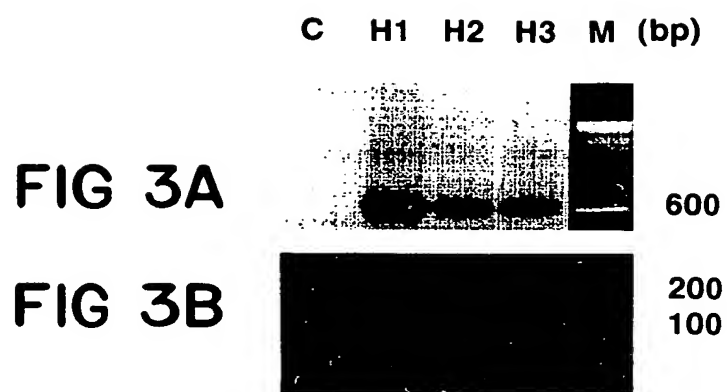
FIG. 2K

Consensus BDV JCT BDV Briese	TRCCCTTCATCAACCCGGGTATAGTGGAGATTGAAGTGTCTRGAATTAATAGCAAGTAYCATGCAGTATCGGAGGCGCYAATATGGATCTGT .A.....A.....A.....T.....T..... .G.....G.....C.....C.....	7920 7920 7920
Consensus BDV JCT BDV Briese	ACATCGCTGCTGCMARCTCTGTGGCGTAAAGCCACACAGTTTGTGTGAGAAACAACGACTTTACGGCCGCGCCACCATGGTT .A.....A.....A..... .C.....G.....	8010 8010 8010
Consensus BDV JCT BDV Briese	GTTATTCCCTTCTTGGTCTAAGTCACGCAATCAATCACAGTCTCTAAGATGGTAGTRCGGAAGCTGAAGCTMTGTCTCTGTATATAT .A.....A.....A.....G.....A..... .A.....A.....C.....	8100 8100 8100
Consensus BDV JCT BDV Briese	ACCCACAGTCGATCCCGCGGTGCTCTCGACCTGTGCCAYCTRCCAGCAYTAACATAATCCTAGTGTCTGGCGGTGACCCAGCGTACT .A.....A.....C.....C.....T..... .T.....T.....	8190 8190 8190
Consensus BDV JCT BDV Briese	AYGAGCGATTACTTGAGATGGACCTRTGCGGGGCTGTGTCAAGTCGMPYGATATCCCCCATTCYCTRGCTGSCAGAACGCACAGGGGT .C.....A.....A.....C.....C.....C..... .T.....G.....A.....C.....T.....G.....	8280 8280 8280
Consensus BDV JCT BDV Briese	TCCARTRGCCAGACGCTGGTCCAGGTGTRATTAGACTYGACARGTTAGAGTCRGTTTGTATTAYGCYACCCCTGTTRGAGGARCTAG .A..A.A.....G.....T.....A.....G.....C.....G..... .G..G.G.....A.....C.....G.....A.....T.....T.....A.....A.....	8370 8370 8370
Consensus BDV JCT BDV Briese	AGTTTAATGCTAYCTAGACTCTGAGTTRGTTGAYATTAGTGATATGTGCTGCCCTCCCYTAGCGACACCCTGTAGGCCCTWTCAGGC .G..G..C.....A.....T.....C.....A..... .A..A..T.....G.....C.....T.....T.....	8460 8460 8460
Consensus BDV JCT BDV Briese	CARTRTATCGGAGCTTACAGTCGTTTCAGGTAGCCTTAATGGACAACATATAGTTTGTMTATGGACCTCATYATGCCGGRSTGGACA .G..G.....A.....A.....C.....C.....G..GG..... .A.A.....C.....T.....A..AC.....	8550 8550 8550

FIG. 2L

Consensus	TYAGGCCCTCAGGARTTTGAYGARTGCTTGTGGTRGGRCAGCAYATCCTCGGYCAGCCCCGTCCCTAGTRGAGGTTGTTTACTACG	8640
BDV JCT	.C.....G....T..A.....G..G....T.....T.....G.....G.....	8640
BDV Briese	.T.....A.....C..G.....A..A.....C.....C.....A.....G.....	8640
Consensus	TTGGAGTTGTRGGAAGCGYCCTGCTGTAGCGAGGCATCCSTGGTCAGCAGATCTTAAGCGAATYACTGTRGGGGGCGRGCKCCCTGCC	8730
BDV JCTG.....T.....C.....C.....C.....C.....A.....A.....G.....	8730
BDV BrieseA.....C.....G.....T.....G.....G.....G.....T.....	8730
Consensus	CYTCTGCTGCYRGAYTGGGTGATGAGGATTGTCRGGGGTCTCTGYTGGTTGGGCTCCYGGCTGGRTTGACGCAGTTTGTGTRRTTGATT	8820
BDV JCT	.T.....TG..C.....G.....C.....C.....C.....A.....G.....G.....G.....	8820
BDV Briese	.C.....CA..T.....A.....T.....T.....G.....A.....A.....A.....	8820
Consensus	RAGRTYRAGCCAYCTACTRCCCTATTCTTAAAAAACCATAYGTCAGTGGTGCAGTGCTTGGGYTTGGTTGCTTTGTGTAGCGCKTT	8910
BDV JCT	G..G..TG.....T.....G.....C.....C.....T.....T.....T.....T--	8908
BDV Briese	A..A.CA.....C.....A.....T.....C.....C.....G.....G..	8910

FIG. 2M



Strain V	10	20	30	40	50	60	70	80	90	100	
	ATGGCAACGCGACCATCGAGTCTGGTCTGACTCCCTGGAGGACGAAGAAGATCCCCAGACACTACGACGGGAACGACCCGGGGTCAACAAGACCACGGAAGG										100
GA.....										100
G.....										100
GA.....										100
C6BVG.....										100
Strain V	110	120	130	140	150	160	170	180	190	200	
	TCCCAAGGAATGCATTGACCCCAACCAAGTAGACCAGCTCCTGAAGGACCTCAGGAAGACCCCTCCATGATCTCAGAGCCAGACCGAAGGGAAGGGA										200
										200
										200
										200
C6BVG.....										200
Strain V	210	220	230	240	250	260	270	280	290	300	
	GCAGCTGTCGAATGATGAGCTAATCAAGAAGTTAGTGACGGAGCTGGCCGAGAATAGCATGATCGAGGCTGAGGAGGTGCGGGGCACTCTTGGAGACATC										300
										300
										300
										300
C6BVA.....										300
Strain V	310	320	330	340	350	360	370	380	390	400	
	TCGGCTCGTATCGAAGGCAGGGTTTGAGTCCCTGTCCGCCCTCCAAGTGGAAACCATCCAGACAGCTCAGGGGTGGGATCACTCCGACAGCATCAGGATCC										400
										400
										400
										400
C6BVC.....										400

FIG. 4A-1

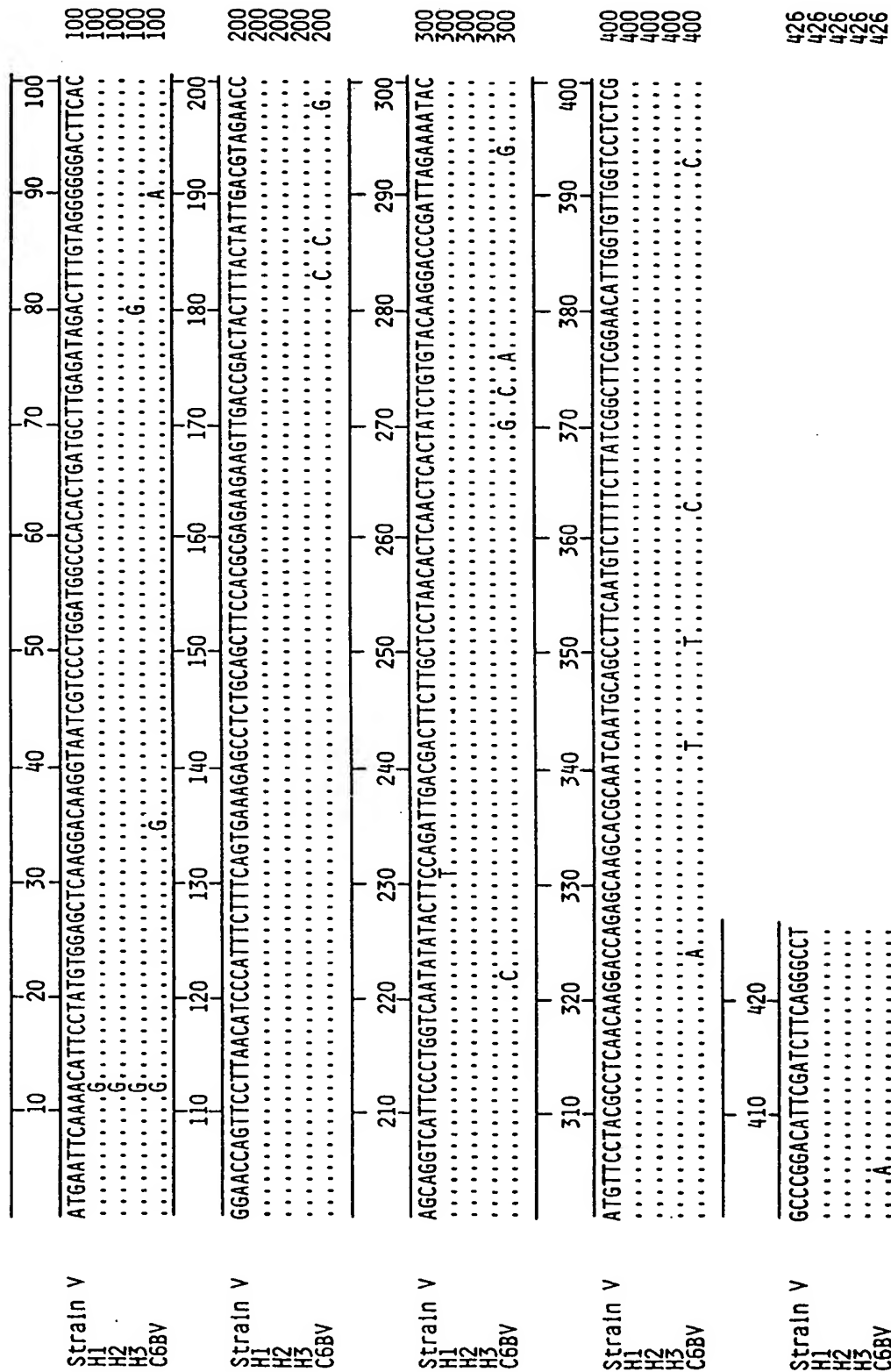


FIG. 4B

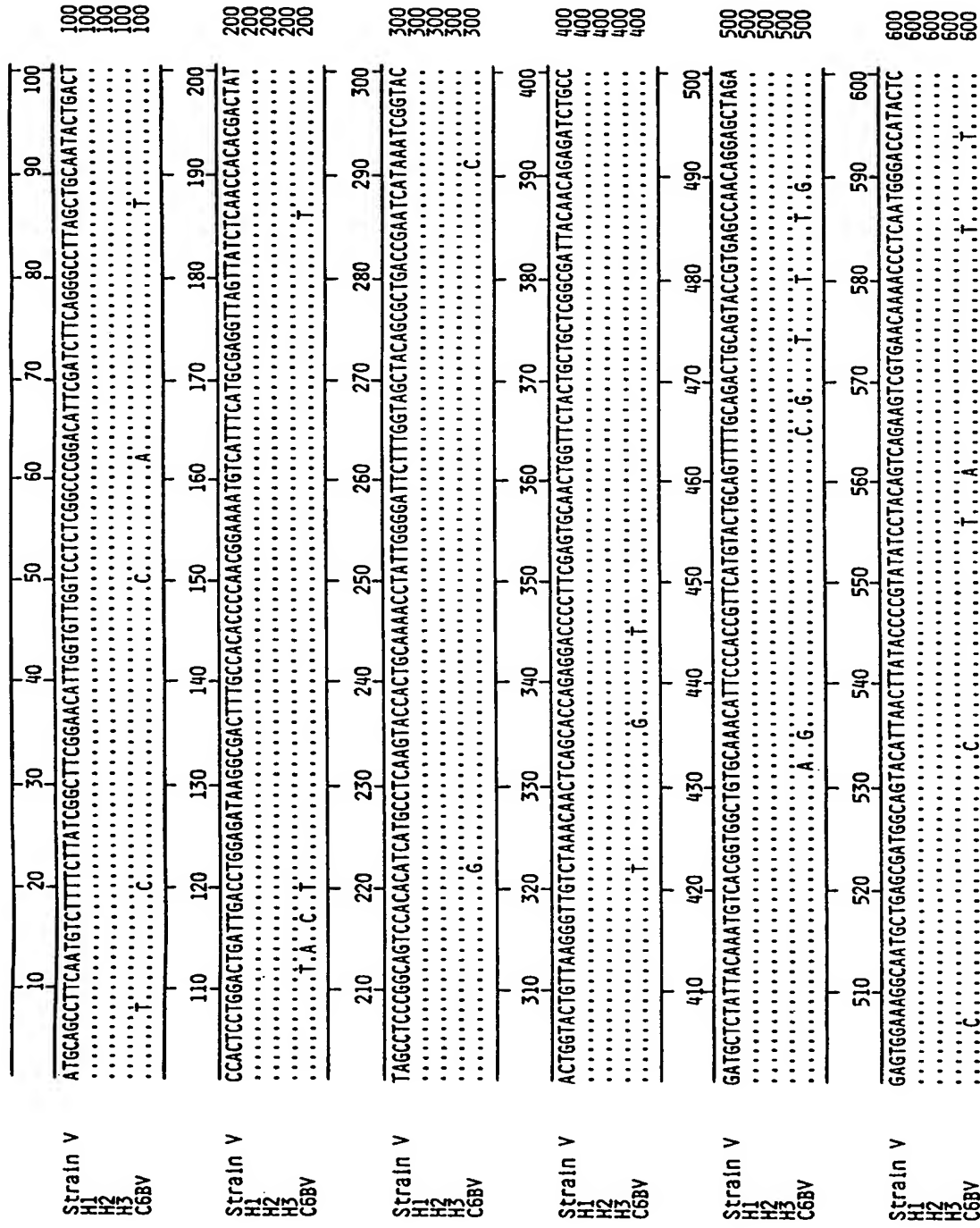


FIG. 4C-I

Strain V	610	620	630	640	650	660	670	680	690	700	700
H1	TGCACTCATCCTCTAAGATAGTTTCCTTCGATGAATTTAGCGGTTTCATCTCCCTAACGAATGGTAGTTACCGAGGCTCATCAATCAATGTGACGTGTG										700
H2										700
H3										700
C6BVC.....			G.....						700
Strain V	710	720	730	740	750	760	770	780	790	800	800
H1	CAAATACACGTCGTCTGCCGGCCCCAGGTTGAAAAGCGCGGTAGGACACCCAGCAGATTGAGTATCTAGTTCAACAGCTTAGGCCACACACTGAAGA										800
H2										800
H3										800
C6BVT.....T...A...G.....G.....T...T...A...C.....C.....T.....T.....										800
Strain V	810	820	830	840	850	860	870	880	890	900	900
H1	TGCATGGGAGGACTGTGAGATCCTCCAGTCTCTGCTCTAGGGGTGTTGGTACTGGGATCGCAAGTGCTTCTCAATTTTGAGGAGCTGGCTCAACCAC										900
H2										900
H3										900
C6BVG.....		A.....T.....G.....C.....G.....					900
Strain V	910	920	930	940	950	960	970	980	990	1000	1000
H1	CCTGACATCATCGGGTATATAGTTAATGGAGTTGGGTTGTCCTGGCATGCCATCGTGTATATGTCACGTTTCATGGCGTGGGAATGAGTCCACCTATTACC										1000
H2										1000
H3										1000
C6BVT.....		A.....T.....G.....C.....G.....					1000
Strain V	1010	1020	1030	1040	1050	1060	1070	1080	1090	1100	1100
H1	CTCCAGTAGATTACAATGGCGGAAGTACTTCTCGAATGATGAGGGAAGGTTACAACAACACCCCGAGGCAAGGCCAGGGCTTAAGCGGGTCATGTG										1100
H2										1100
H3										1100
C6BVA.....		T.....G.....C.....						1100
Strain V	1110	1120	1130	1140	1150	1160	1170	1180	1190	1200	1200
H1	GTTCCGAGGTACTTCTAGGACAGTAGGGTCTGGGGTGAACCCGAGGAGGATTCGGTACAATAAGACCTCACATGACTACCACCTGGAGGAGTTTGAG										1200
H2										1200
H3										1200
C6BVT.....T.....T.....A.....				1200

FIG. 4C-2

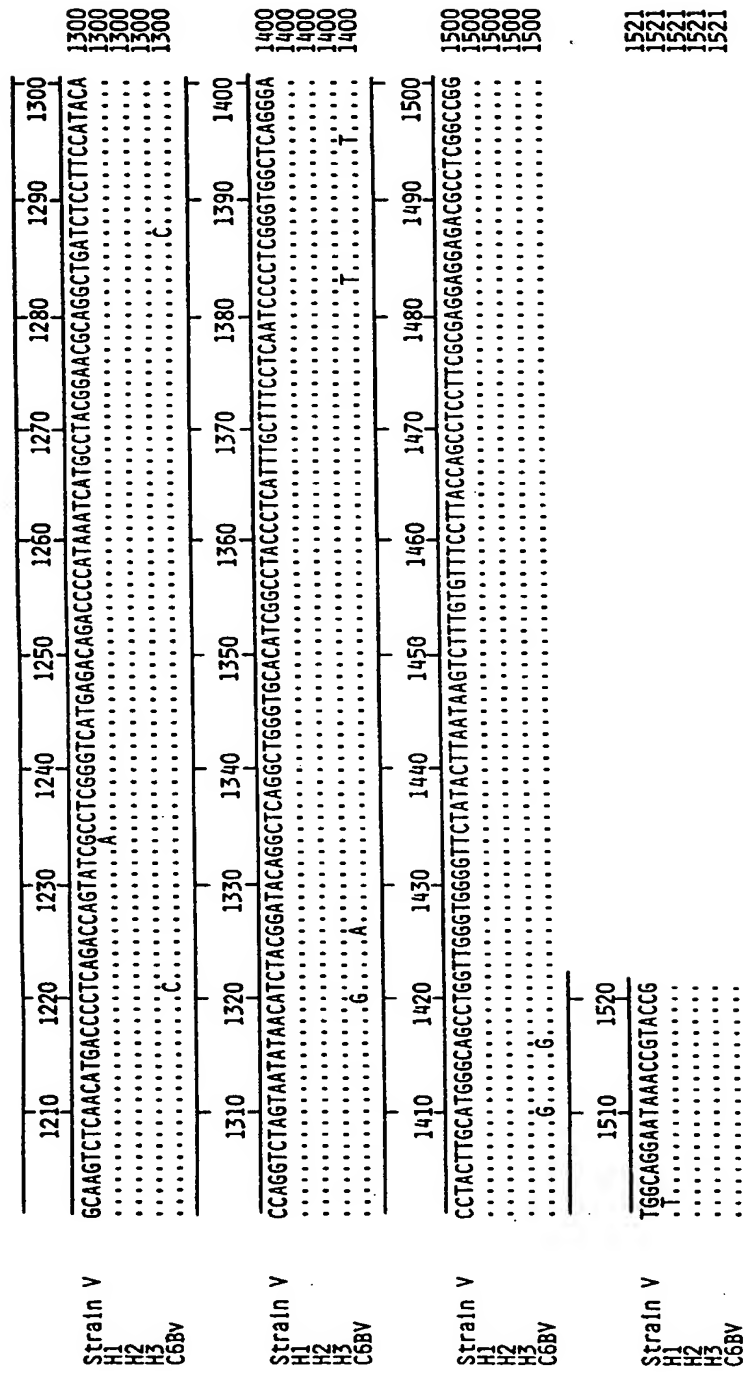


FIG. 4C-3

C6BV p40Int	50
H1 p40Int	50
H2 p40Int	50
H3 p40Int	50
StrainV p40Int	50
Consensus	TTCA	ACAGT	AACGCC	AGC	CTTGTGTTTC	TATGTTTGCT	AATCCCAGGA	50
C6BV p40Int	100
H1 p40Int	100
H2 p40Int	100
H3 p40Int	100
StrainV p40Int	100
Consensus	CTGCACGCTG	CGTTTGTTC	CGGAGGGGTG	CCTCGTGAAT	CTACCTGTC			100
C6BV p40Int	150
H1 p40Int	150
H2 p40Int	150
H3 p40Int	150
StrainV p40Int	150
Consensus	GACGCCTRTY	ACGCGTGGG	AACAGACTGT	YGTTAAGACT	GRRAGTTTT			150
C6BV p40Int	200
H1 p40Int	200
H2 p40Int	200
H3 p40Int	200
StrainV p40Int	200
Consensus	ACGGGGAAAA	GACRACRCAG	CGTGATCTCA	CCGAGCTGGA	GATCTCCTCT			200
C6BV p40Int	250
H1 p40Int	250
H2 p40Int	250
H3 p40Int	250
StrainV p40Int	250
Consensus	ATMTTCAGCC	ATTGTTGCTC	ATTACTAATW	GGGGTTGTGA	TAGGATCGTC			250
C6BV p40Int	300
H1 p40Int	300
H2 p40Int	300
H3 p40Int	300
StrainV p40Int	300
Consensus	RTCTAAGATY	AAAGCAGRAG	CCGAGCAGAT	CAAGAAAAGG	TTTAAACTA			300

FIG. 5A-I

C6BV p40IntT.....T	350
H1 p40IntT.....C	350
H2 p40IntG.....C	350
H3 p40IntT.....C	350
StrainV p40IntT.....C	350
Consensus	TGATGGCAGC CKTAAACCGG CCATCCCATG GTGAGACTGC TACACTACTY	350
C6BV p40IntG.....	400
H1 p40IntA.....	400
H2 p40IntA.....	400
H3 p40IntA.....	400
StrainV p40IntA.....	400
Consensus	CAGATGTTTA ATCCACATGA GGCTATAGAT TGGATTAACG GCCARCCCTG	400
C6BV p40IntT.....	450
H1 p40IntCT.....	450
H2 p40IntTT.....	450
H3 p40IntTT.....	450
StrainV p40IntTT.....	450
Consensus	GGTAGGCTCC TTTGTGTTGY CTCTACTAAC TACAGACTTT GAGTCCCCAG	450
C6BV p40IntC.....G.....	500
H1 p40IntCT.....C.....G.....	500
H2 p40IntTT.....C.....G.....	500
H3 p40IntTT.....C.....G.....	500
StrainV p40IntTT.....C.....G.....	500
Consensus	GTAAAGAATT YATGGAYCAG ATTAARCTTG TCGCAAGTTA TGORCAGATG	500
C6BV p40IntT.....	550
H1 p40IntCT.....	550
H2 p40IntCT.....	550
H3 p40IntCT.....	550
StrainV p40IntCT.....	550
Consensus	ACTACGTACA CTACTATAAA GGAGTACCTC GCAGAATGYA TGGATGCTAC	550
C6BV p40IntT.....	571
H1 p40IntT.....	571
H2 p40IntT.....	571
H3 p40IntT.....	571
StrainV p40IntC.....	571
Consensus	CCTTACAATC CCYGTAGTTG C	571

FIG. 5A-2

Consensus	TGACCATGAG CTCAACGGGY CTAAGCAYC TTCTTAACCG GCTATCACAT	50
p180fragC.....C.....T.....	50
H1 p180T.....T.....C.....	50
H2 p180T.....T.....C.....	50
H3 p180T.....T.....C.....	50
Strain 5 p180T.....T.....C.....	50
Consensus	ACTATCACTA AGGGTGACTC CTTTGTATT AAQYMGAYT ATAGTCCTG	100
p180fragT.....A.....T.....C.....	100
H1 p180C.....T.....C.....T.....	100
H2 p180C.....T.....C.....T.....	100
H3 p180C.....T.....C.....T.....	100
Strain 5 p180C.....T.....C.....T.....	100
Consensus	GTGCAACGGT TTCCGACCAG AACTRCARGC CCCAMTCTGT CGTCAGTTGG	150
p180fragA.....A.....C.....	150
H1 p180G.....G.....A.....	150
H2 p180G.....G.....A.....	150
H3 p180G.....G.....A.....	150
Strain 5 p180G.....G.....A.....	150
Consensus	ATCAGATGTT CAATTGCGGG TACTTCTTCA GGACTGGGTG CACACTGCCA	200
p180frag	200
H1 p180	200
H2 p180	200
H3 p180	200
Strain 5 p180	200
Consensus	TGCTTTACCA CGTTTATTAT TCARGACAGR TTCAACCCGC CCTATTCQYI	250
p180fragG.....A.....T.....	250
H1 p180A.....G.....C.....	250
H2 p180A.....G.....C.....	250
H3 p180A.....G.....C.....	250
Strain 5 p180A.....G.....C.....	250
Consensus	GTGGTGAG CCCGTTGAAG ACGGMYAC ATGCGCGGTT GGGACTAARA	300
p180fragC.....T.....C.....G.....	300
H1 p180A.....A.....T.....A.....	300
H2 p180A.....A.....T.....A.....	300
H3 p180A.....A.....T.....A.....	300
Strain 5 p180A.....A.....T.....A.....	300

FIG. 5B-I

Consensus	CAATGGGGA GGGATGAGG CAGAACTAT GGACAATCT TACGAGCTGC	350
p180fragA.....T.....T.....	350
H1 p180G.....C.....	350
H2 p180G.....C.....	350
H3 p180G.....C.....	350
Strain 5 p180G.....C.....	350
Consensus	TGGGAGATAA TTGCTCTTCG GGAAATTAAC GTGACGTTA ATATACTAGG	400
p180fragT.....	400
H1 p180C.....	400
H2 p180C.....	400
H3 p180C.....	400
Strain 5 p180C.....	400
Consensus	CCARGGTGAT AATCAGACAA TCATYRTACA TAAATCTGCA AGCCAAAATA	450
p180frag	...G.....TG.....	450
H1 p180	...A.....CA.....	450
H2 p180	...A.....CA.....	450
H3 p180	...A.....CA.....	450
Strain 5 p180	...A.....CA.....	450
Consensus	ATCAGCTATT AGCGGAGCGA GCATTTGGG GYYTGACAA GCATGCTAGA	500
p180frag	..T.....T..G..A..TT.....	500
H1 p180	..C.....C..A..G..CC.....	500
H2 p180	..C.....C..A..G..CC.....	500
H3 p180	..C.....C..A..G..CC.....	500
Strain 5 p180	..C.....C..A..G..CC.....	500
Consensus	TTAGCTGGCC ATAACCTTAA GGTAGARGAA TGTGGGTGT CAGATTGTCT	550
p180fragT.....A.....T.....	550
H1 p180C.....G.....C.....	550
H2 p180C.....G.....C.....	550
H3 p180C.....G.....C.....	550
Strain 5 p180C.....G.....C.....	550
Consensus	GTATGAGTAT GGAAAGAAGC TTTCTTCCG TGGTGTACCT GTCCGAGGCT	600
p180fragC.....A.....	600
H1 p180T.....G.....	600
H2 p180T.....G.....	600
H3 p180T.....G.....	600
Strain 5 p180T.....G.....	600

FIG. 5B-2

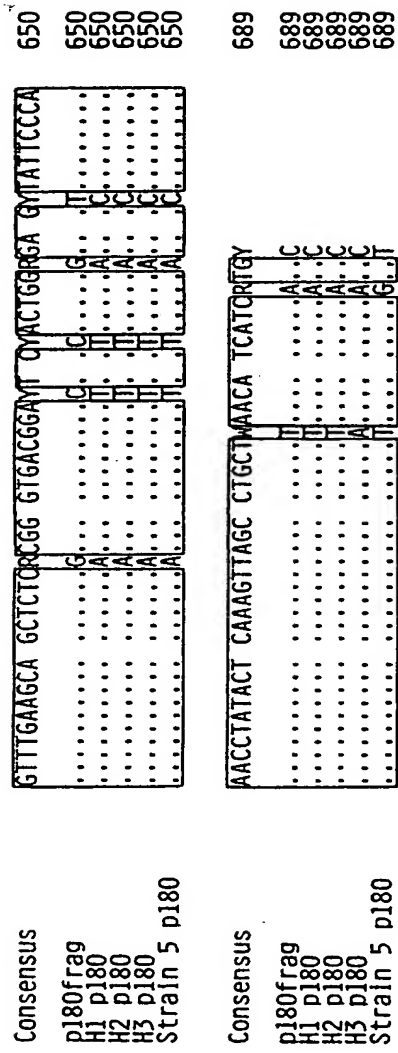


FIG. 5B-3

	p24					p16			p56														
	4	26	34	127	194	12	27	108	3	7	17	21	220	234	242	243	245	282	296	326	412	465	501
C6BV	G	S	I	H	A	G	D	E	L	S	A	Q	A	V	S	L	R	M	G	A	A	L	W
H1	E	-	V	Y	T	D	-	D	P	F	V	R	T	A	P	R	L	V	S	T	T	P	L
H2	-	-	V	-	T	-	-	D	P	F	V	R	T	A	P	R	L	V	S	T	-	P	-
H3	E	-	V	-	T	-	G	D	P	F	V	R	T	A	P	R	L	V	S	T	-	P	-
Strain V	R	P	V	-	T	D	-	D	P	F	V	R	T	A	P	R	L	V	S	-	-	P	-

FIG. 6A

	p24					p16					p56				
	C6BV	H1	H2	H3	Strain V	C6BV	H1	H2	H3	Strain V	C6BV	H1	H2	H3	Strain V
C6BV		16	14	14	17		17	16	17	16		67	65	65	64
H1	4		2	1	5	2		2	3	3	15		2	2	3
H2	2	2		2	3	1	1		1	1	13	2		0	1
H3	3	1	1		5	2	2	1		2	13	2	0		1
Strain V	4	3	2	2		1	1	0	1		12	3	1	1	

FIG. 6B

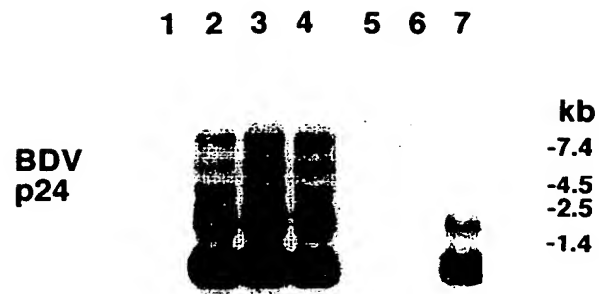


FIG. 7A

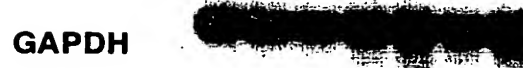


FIG. 7B



1 2 3 4 5 6 7

FIG. 7C

MATEPSSLVDSLEDEEDPQTLRRERSGSPRPRKVPRNALTQVDQQLKDLRKNPSMISDP
DQRTGREQLSNDELIKLVTELAENSMIEAEVEVRGTLGDISARIEAGFESLSALQVETIQT
AQRCDYSDSIRILGENIKILDRSMKTMETMKLMMKEKVDLLYASTAVGTSAPMLPSHP
APPRIYPQLPSAPTDEWDIIP

FIG. 8A

MATGPSSLVDSLEDEEDPQTLRRERSGSPRPRKVPRNALTQVDQQLKDLRKNPSMISDP
DQRTGREQLSNDELIKLVTELAENSMIEAEVEVRGTLGDISARIEAGFESLSALQVETIQT
AQRCDHSDSIRILGENIKILDRSMKTMETMKLMMKEKVDLLYASTAVGTSAPMLPSHP
APPRIYPQLPSAPTDEWDIIP

FIG. 8B

MATEPSSLVDSLEDEEDPQTLRRERSGSPRPRKVPRNALTQVDQQLKDLRKNPSMISDP
DQRTGREQLSNDELIKLVTELAENSMIEAEVEVRGTLGDISARIEAGFESLSALQVETIQT
AQRCDHSDSIRILGENIKILDRSMKTMETMKLMMKEKVDLLYASTAVGTSAPMLPSHP
APPRIYPQLPSAPTDEWDIIP

FIG. 8C

MNSKHSYVELKDKVIVPGWPTLMLEIDFVGGTSRNQFLNIPFLSVKEPLQLPREKKLTDY
FTIDVEPAGHSLVNIYFQIDDFLLLTLSLSVYKDPIRKYMFLRLNKDQSKHAINAAFNVF
SYRLRNIGVGPLGPDIRSSGP

FIG. 9A

MNSKHSYVELKDKVIVPGWPTLMLEIDFVGGTSRNQFLNIPFLSVKEPLQLPREKKLTDY
FTIDVEPAGHSLVNIYFQIDDFLLLTLSLSVYKDPIRKYMFLRLNKDQSKHAINAAFNVF
SYRLRNIGVGPLGPDIRSSGP

FIG. 9B

MNSKHSYVELKDKVIVPGWPTLMLEIGFVGGTSRNQFLNIPFLSVKEPLQLPREKKLTDY
FTIDVEPAGHSLVNIYFQIDDFLLLTLSLSVYKDPIRKYMFLRLNKDQSKHAINAAFNVF
SYRLRNIGVGPLGPDIRSSGP

FIG. 9C

MQPSMSFLIGFGTLVLVLSARTFDLQGLSCNTDSTPGLIDLEIRRLCHTPTENVISCEVSYL
NHTTISLPAVHTSCLKYHCKTYWGFFGSYADRINRYTGTVKGCLNNSAPEDPFECNW
FYCCSAITTEICRCSITNVTVAVQTFFPFMYCSFADCS TVSQELES GKAMLS DGS TLTYT
PYILQSEVVNKTILNGTILCNSSSKIVSFDEFRRSYSLTNGSYQSSINVT CANYTSSCRPRL
KRRRRDTQIEYLVHKLRLKDAWEDCEILQSLLLGVFGTGIASASQFLRSWLNHPDII
GYTVNGVGVVWQCHRVNVTFMTWNESTYPPVDYNGRKYFLNDEGR LQTNTPEARPG
LKRVMWFGRYFLGT VGS GVKPRRIRYNKTSHDYHLEEF EASLNMTPQTSITSGHETDPI
NHA YGTQADLLPYTRSSNITSDTGS GWVHIGLPSFAFLNPLGWLRDLLA WAAWLGGV
LYLISLCVSLPASFAARRRLGRLQE

FIG. 10A

MQPSMSFLIGFGTLVLVLSARTFDLQGLSCNTDSTPGLIDLEIRRLCHTPTENVISCEVSYL
NHTTISLPAVHTSCLKYHCKTYWGFFGSYADRINRYTGTVKGCLNNSAPEDPFECNW
FYCCSAITTEICRCSITNVTVAVQTFFPFMYCSFADCS TVSQELES GKAMLS DGS TLTYT
PYILQSEVVNKTILNGTILCNSSSKIVSFDEFRRSYSLTNGSYQSSINVT CANYTSSCRPRL
KRRRRDTQIEYLVHKLRLKDAWEDCEILQSLLLGVFGTGIASASQFLRSWLNHPDII
GYTVNGVGVVWQCHRVNVTFMTWNESTYPPVDYNGRKYFLNDEGR LQTNTPEARPG
LKRVMWFGRYFLGT VGS GVKPRRIRYNKTSHDYHLEEF EASLNMTPQTSITSGHETDPI
NHA YGTQADLLPYTRSSNITSDTGS GWVHIGLPSFAFLNPLGWLRDLLA WAAWLGGV
LYLISLCVSLPASFAARRRLGRWQE

FIG. 10B

10	20	30	40	50
1234567890	1234567890	1234567890	1234567890	1234567890
HIVTSLVFL	CLLIPGLHAA	FVHGVVPRES	YLSPTIRGE	QIVVKTAIFY
GEKTIQRDLT	ELEISSIFSH	CCSLLIGWVI	GSSSKIKAGA	EQIKKRFKIM
MAALNRPSHG	ETATLLQMFN	PHEAIDWING	QFWGSEFVLS	LLTTDFESRG
KEFMDQIKLV	ASYAQMTITYT	TIKEYLAECM	DATLTIPW	

FIG. IIA

10	20	30	40	50
1234567890	1234567890	1234567890	1234567890	1234567890
HIVTSLVFL	CLLIPGLHAA	FVHGVVPRES	YLSPTIRGE	QIVVKTAIFY
GEKTIQRDLT	ELEISSIFSH	CCSLLIGWVI	GSSSKIKAEA	EQIKKRFKIM
MAAVNRPSHG	ETATLLQMFN	PHEAIDWING	QFWGSEFVLS	LLTTDFESRG
KEFMDQIKLV	ASYAQMTITYT	TIKEYLAECM	DATLTIPW	

FIG. IIB

10	20	30	40	50
1234567890	1234567890	1234567890	1234567890	1234567890
HIVTSLVFL	CLLIPGLHAA	FVHGVVPRES	YLSPTIRGE	QIVVKTAIFY
GEKTIQRDLT	ELEISSIFSH	CCSLLIGWVI	GSSSKIKAGA	EQIKKRFKIM
MAALNRPSHG	ETATLLQMFN	PHEAIDWING	QFWGSEFVLS	LLTTDFESRG
KEFMDQIKLV	ASYAQMTITYT	TIKEYLAECM	DATLTIPW	

FIG. IIC

10	20	30	40	50
1234567890	1234567890	1234567890	1234567890	1234567890
TMSSTAL/HL	LNRLSHITIK	GDSFVINLDY	SSWNGFRPE	LQAPICRQLD
QMFNGYFFR	TGCTLPCFTT	FLIQDRNPP	YSLSGEPVED	GVICAVGIKT
MGEGRQKLW	TLITSCWEII	ALREINVTFN	ILQQEDNQTI	IHKASQNN
QLLAERALGA	LYKHARLAGH	NLKVEECOWS	DCLYEYGGKL	FFRGVPVPGC
LKQLSRVIDS	TGELFRNLYS	KLCLTSSC		

50
100
150
200
229

FIG. 12